

Fig. 1a

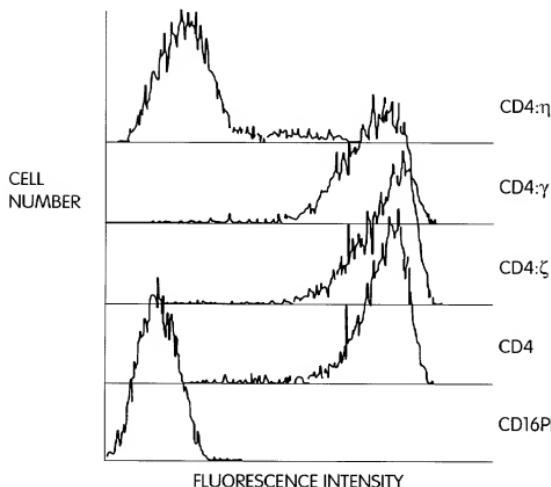


Fig. 1b

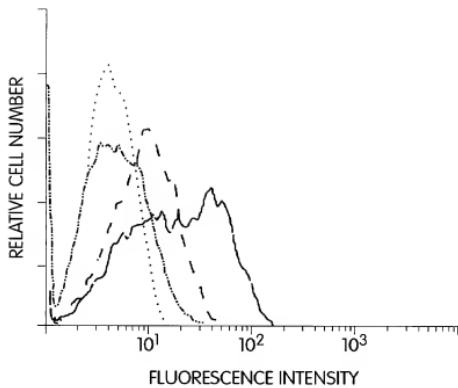


Fig. 2

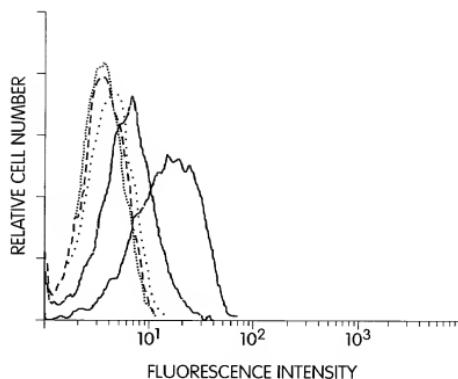


Fig. 3

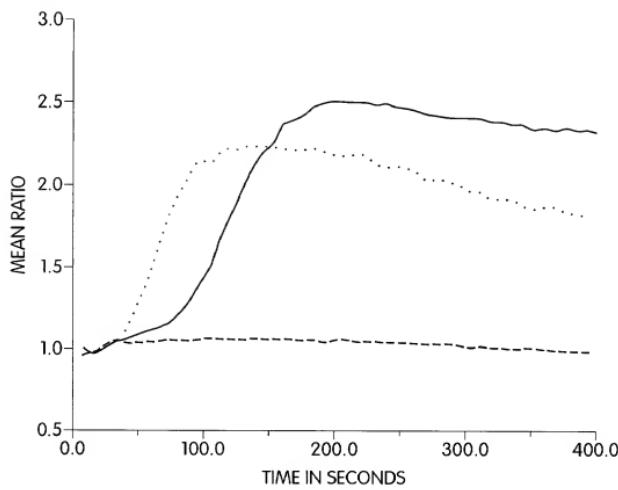


Fig. 4a

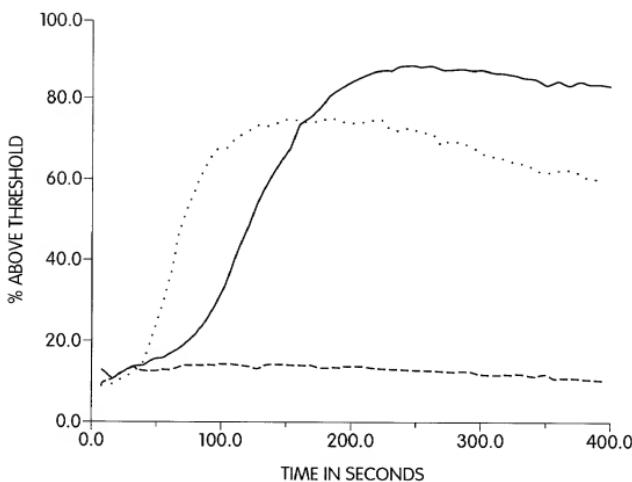


Fig. 4b

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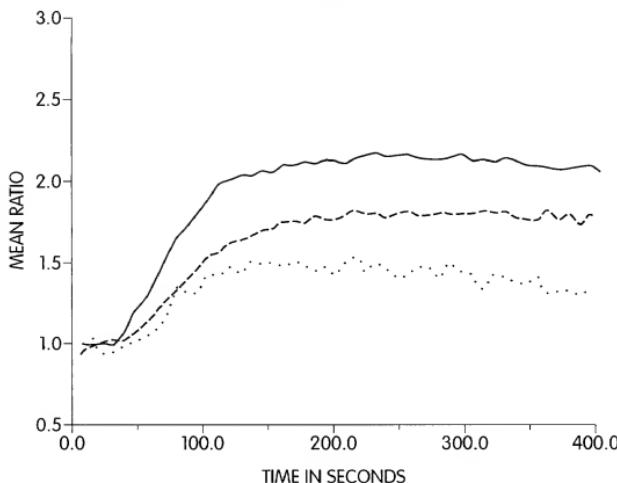


Fig. 4c

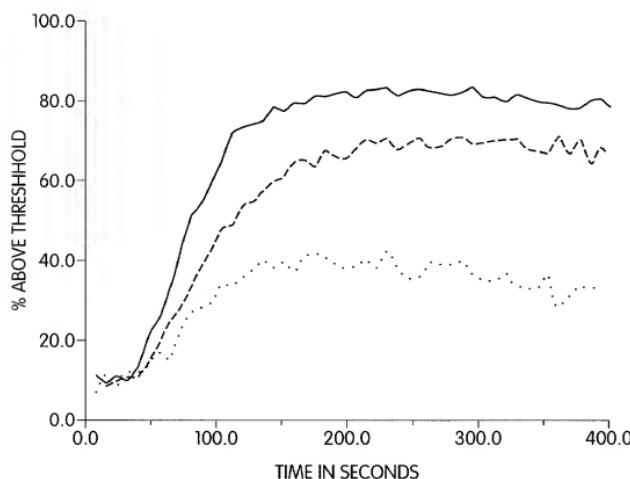


Fig. 4d

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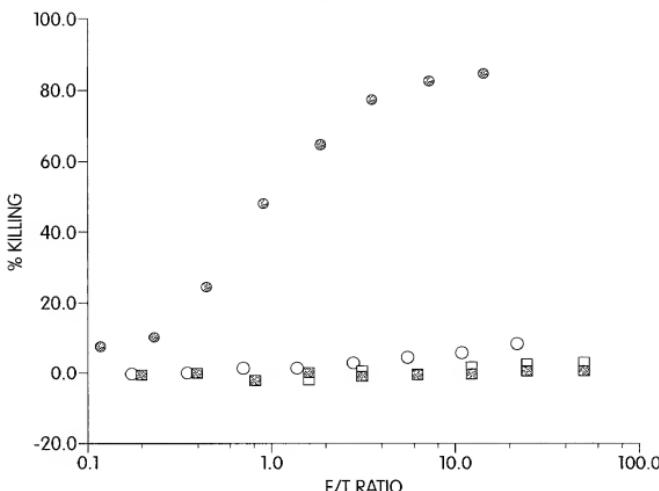


Fig. 5a

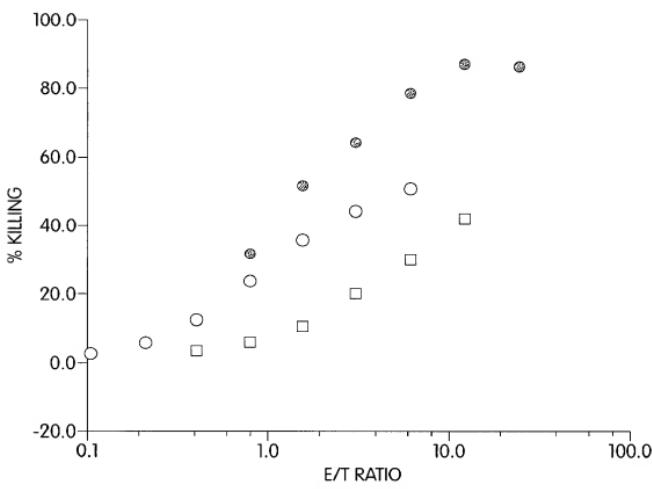


Fig. 5b

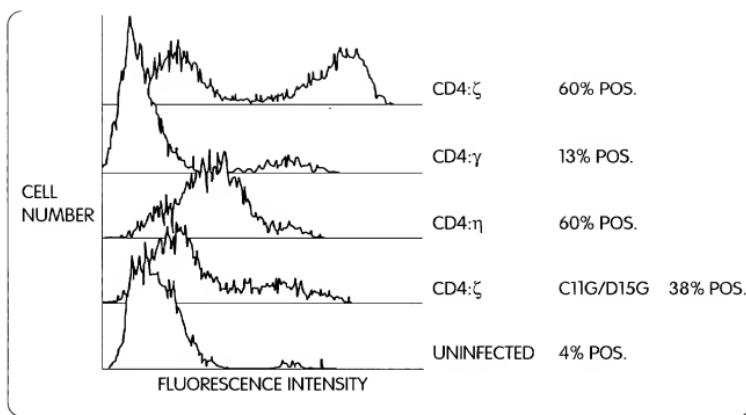


Fig. 5c

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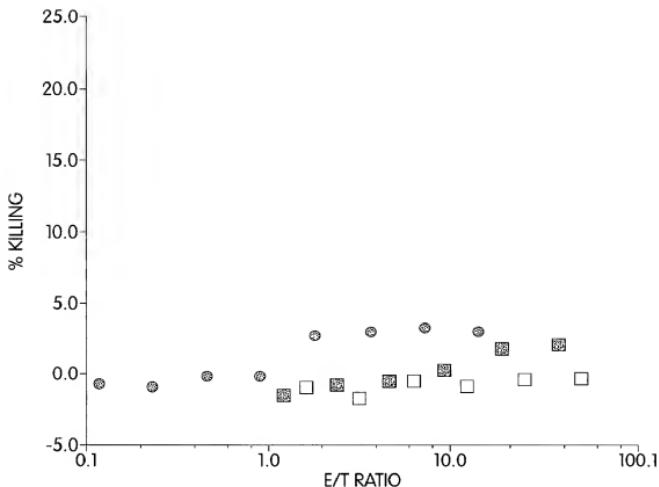


Fig. 6a

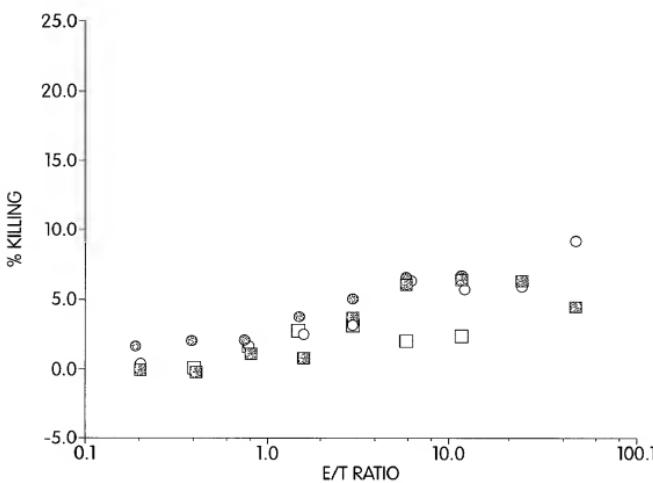


Fig. 6b

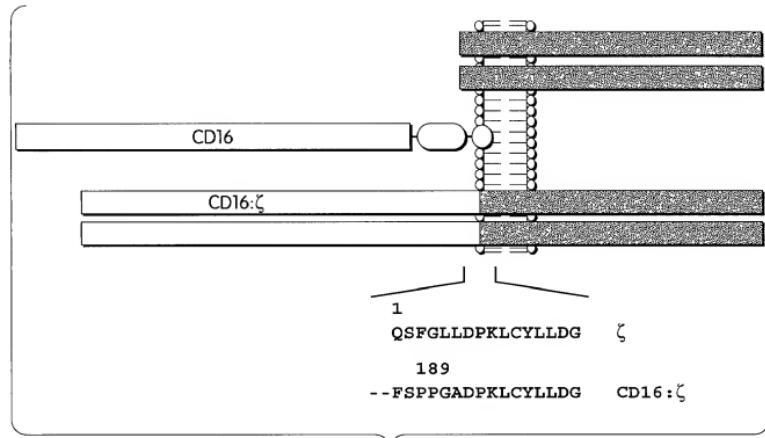


Fig. 7a

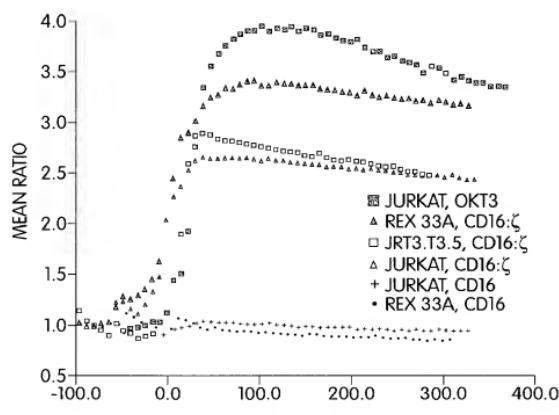


Fig. 7b

F34\* Y51\*

1 QSFGLLDPKL CYLLDGILFI YGVILTAFL RVKFSRSAEP PAYQQGONQL  
 ↓      ↓  
 E60\* D66\*

51 YNELNLGRRE EYDVLDKRRG RDPEMGGKPR RKNPQEGLYN ELQDKMAEA  
 ↓      ↓

G122\* A133\* L139\*

101 YSEIGMKGER RRGKGHDGLY QGLSTATKDT YDALHMQALP PR  
 ↓      ↓      ↓

Fig. 8a

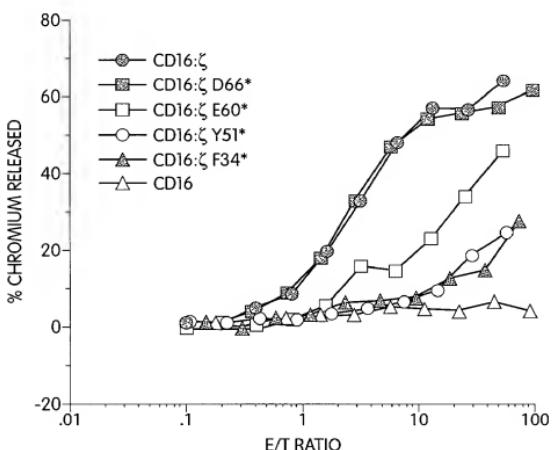


Fig. 8b

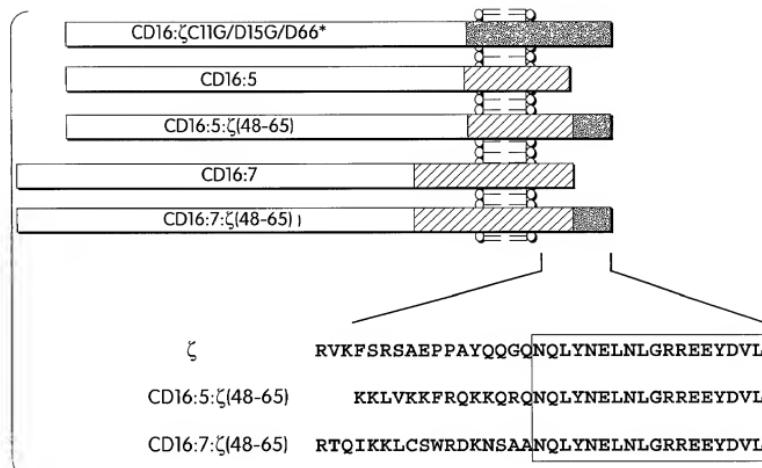


Fig. 9a

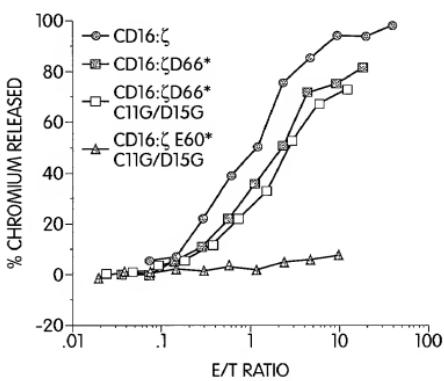


Fig. 9b

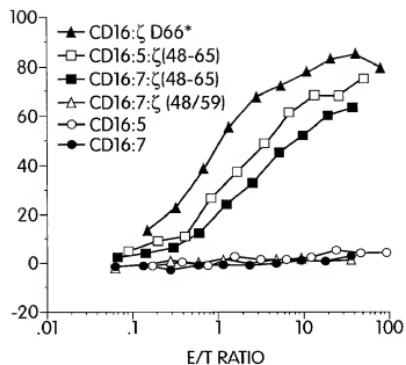


Fig. 9c

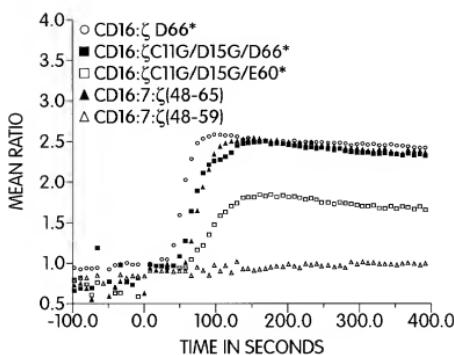


Fig. 9d

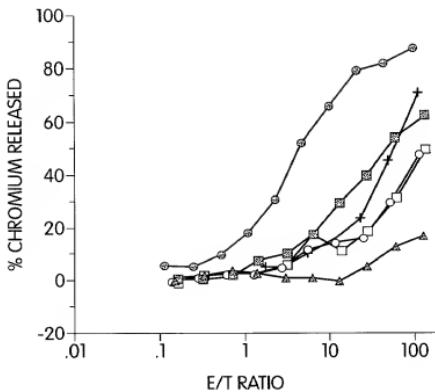


Fig. 10a

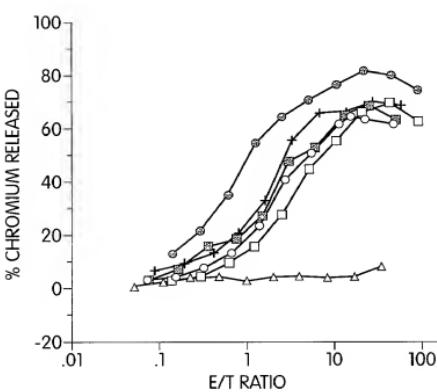


Fig. 10b

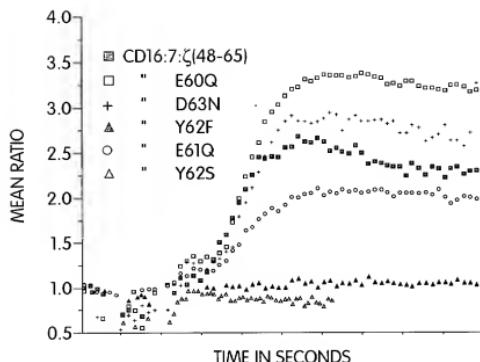


Fig. 10c

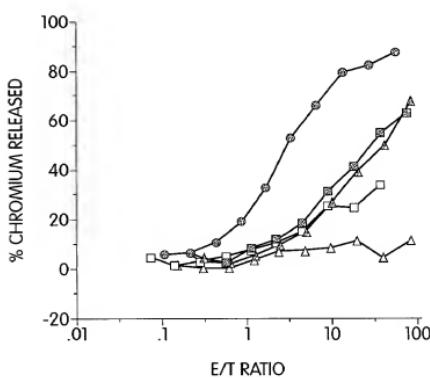


Fig. 10d

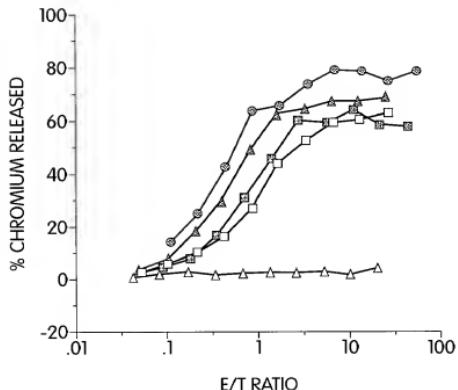


Fig. 10e

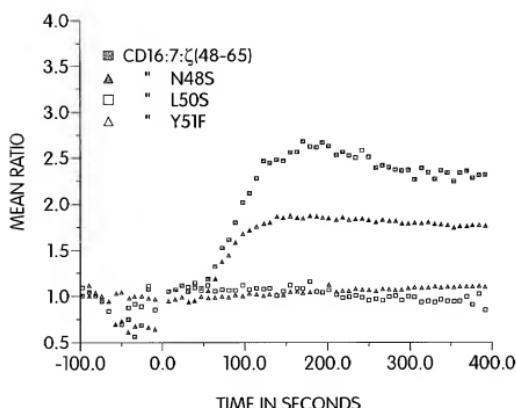


Fig. 10f

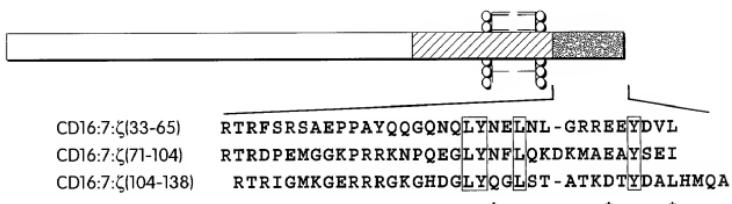


Fig. 11a

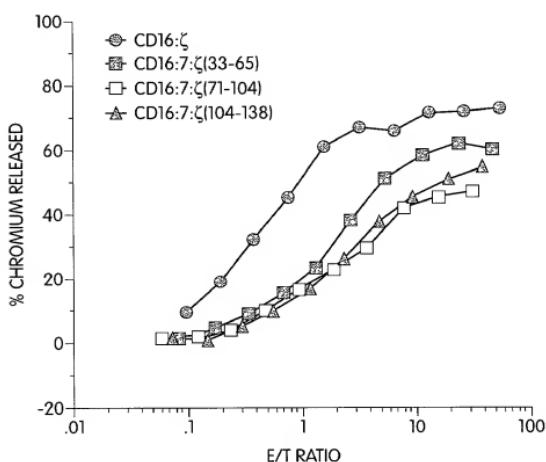


Fig. 11b

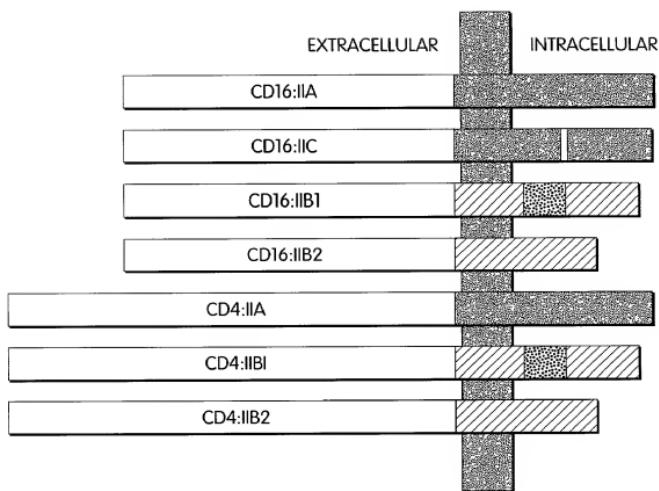


Fig. 12

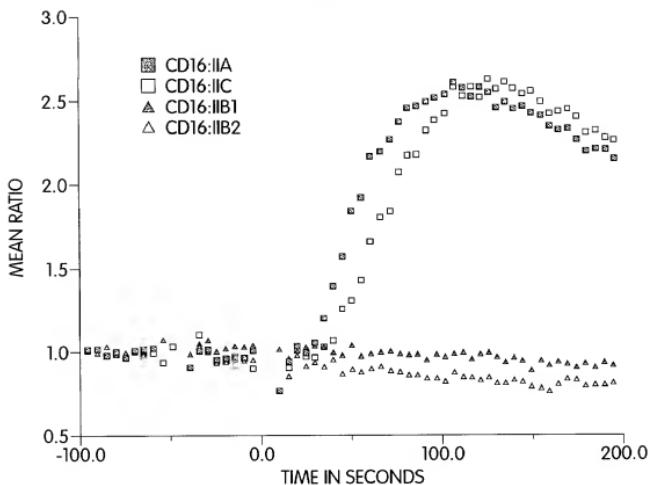


Fig. 13a

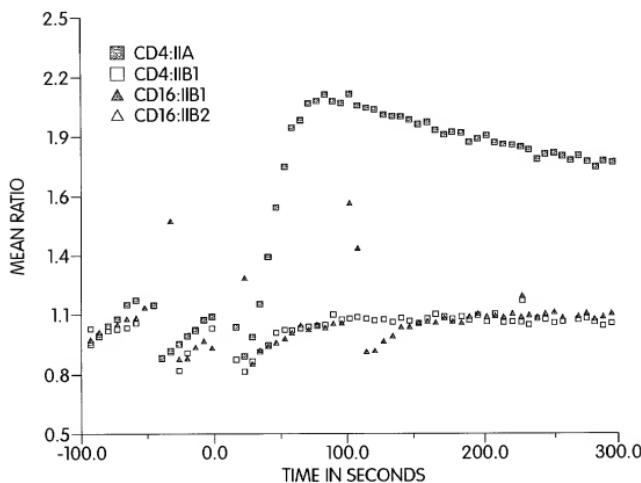


Fig. 13b

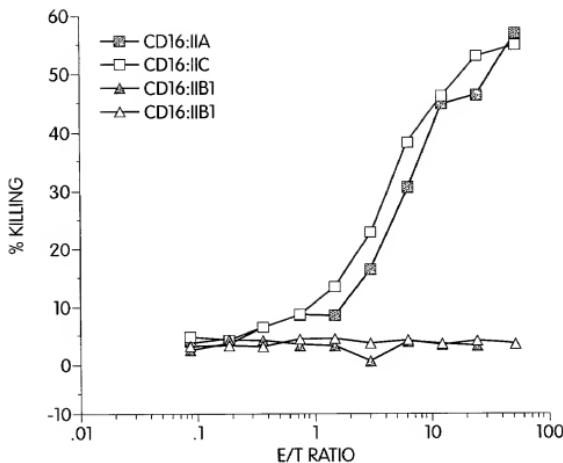


Fig. 14a

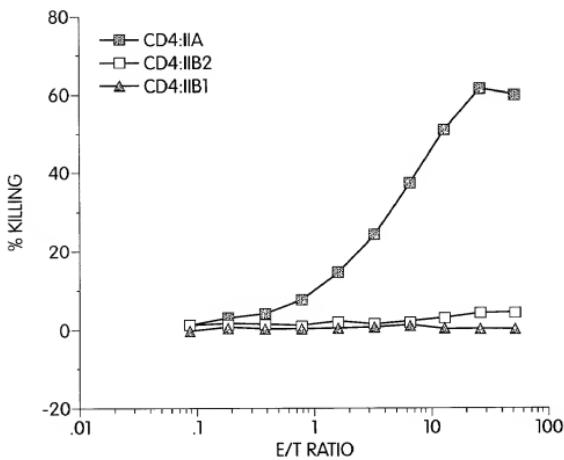


Fig. 14b

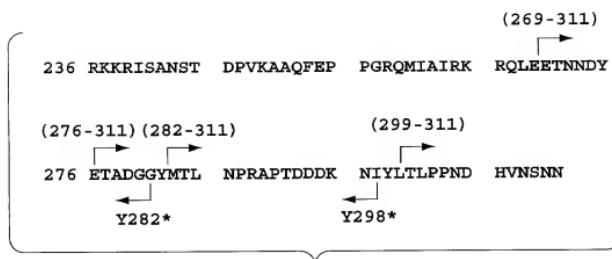


Fig. 15a

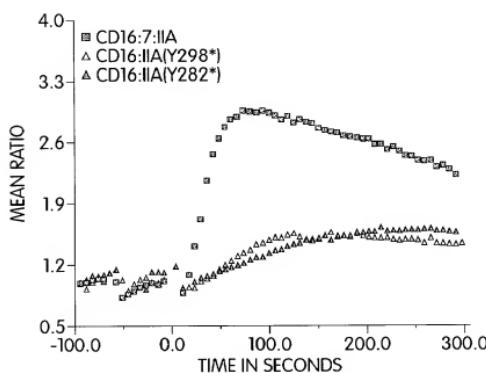


Fig. 15b

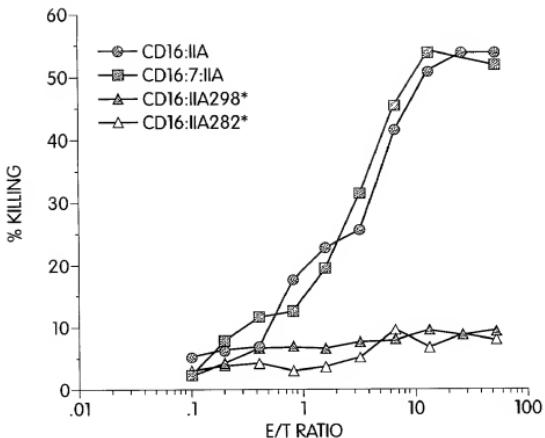


Fig. 15c

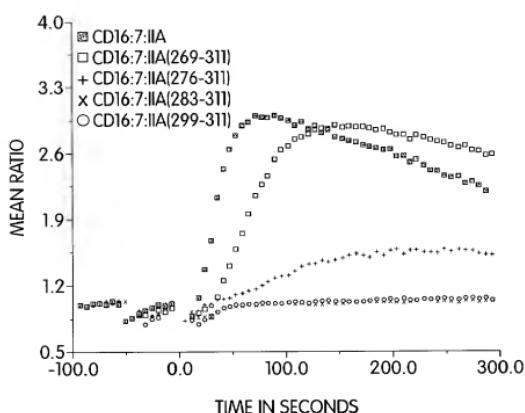


Fig. 15d

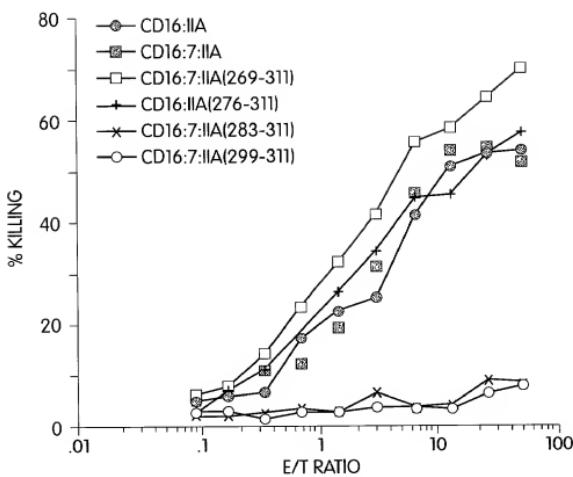


Fig. 15e

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(Seq. ID No: 24)

1	MEHSTFLSGL	VLATLLSQVS	PFKIPIELE	DRVFVNCNTS	ITWVEGTVG
51	LLSDITRLDL	GKRILDPRGI	YRCNGTDIYK	DKESTVQVHY	RMCQSCVEID
101	PATVAGIIVT	DVIATLLLAL	GVFCFAGHET	<u>GRLSGAADTQ</u>	ALLRNDQVYQ
151	<u>PLRDRDDAQY</u>	<u>SHLGGNWARN</u>	K*		

Fig. 16

Seq ID NO: 25)

1	MEQGKGLAVL	ILAIILLQGT	LAQSIKGNH	VKVYDYQEDG	SVLLTCDAEA
51	KNITWFKDGK	MIGFLTEDKK	KWNLGSNAKD	PRGMYQCKGS	QNKSXPQVY
101	YRMCQNCIEL	NAATISGFLF	AEIVSIFVLA	VGVYFIAGQD	<u>GVRQSRASDK</u>
151	<u>QTLLPNDQLY</u>	<u>QPLKDREDDQ</u>	YSHLQGNQLR	RN*	

Fig. 17

(Seq ID No: 26)

1	MPGGLEALRA	LPLLLFLSYA	CLGPGCQALR	VEGGPPSLTV	NLGEEARLTC
51	ENNCRNPNT	WWFLSLSNIT	WPPVPLGPGQ	GTTGQLFFFPE	VNKNTGACTG
101	CQVIENNILK	RSCGTYLVRV	NPVPRPFALM	GEGTKNRIIT	AEGIILLFC
151	VVPGTLLLFR	KRWQNEKFVG	DMPDDYEDEN	LYEGLNLDDC	SMYEDISRGL
201	<u>QGTYQDVGNL</u>	<u>HIGDAQLEKP</u>	*		

Fig. 18

(Seq ID No: 27)

1	MATLVLSSMP	CHWLLFLLLL	FSGEPVPAMT	SSDLPLNFQG	SPCSQIWQHP
51	RFAAKKRSSM	VKFHCYTNHS	GALTWFRKRG	SQQPQELVSE	EGRIVQTQNG
101	SVYTLTIQNI	QYEDNGIYFC	KQKCDSANHN	VTDSCGTELL	VLGFSTLDQL
151	KRNRNLTQDG	ILIQTLLLIL	FIIVPIFL	<u>DKDDGKAGME</u>	EDHTYEGLN
201	<u>DQTTATYEDIV</u>	<u>TLRTGEVKWS</u>	VGEHPGQE*		

Fig. 19

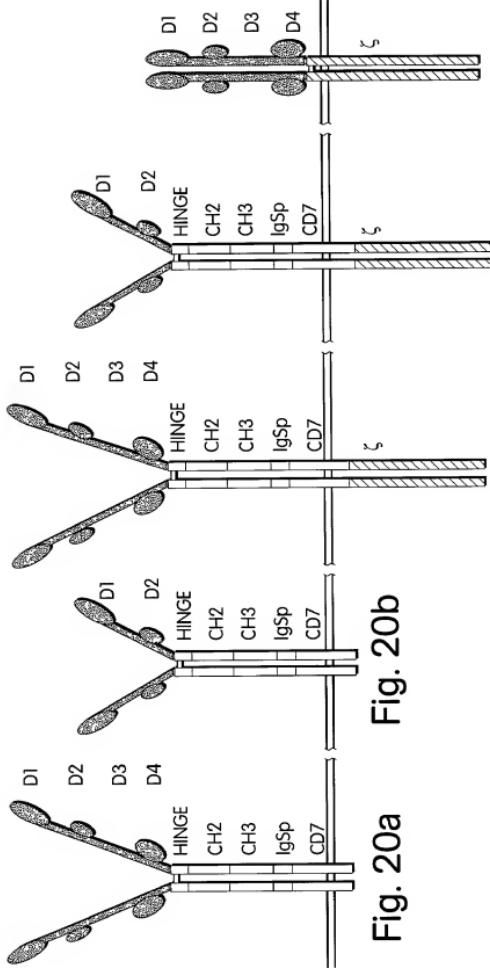


Fig. 20b

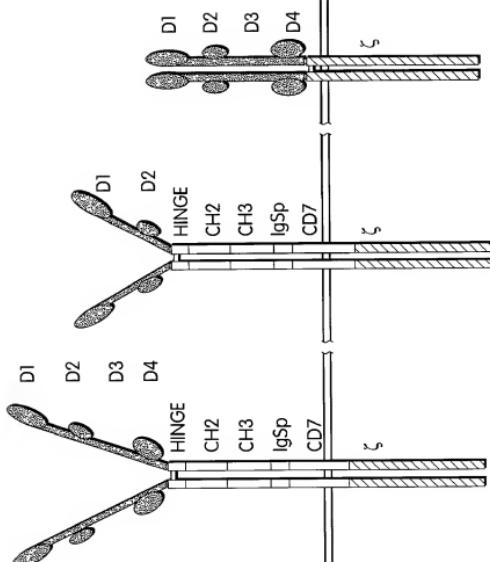


Fig. 20c

Fig. 20d

Fig. 20e

BamHI/BstYI  
 G GAT CCC AAG GCC AGG CTA AAG CCG AAG CGA AGG CCG ACG AGG CTA AGG CAG CAG CAG ATC TG  
 D P K A E A K A E A K A E A D L

Fig. 28

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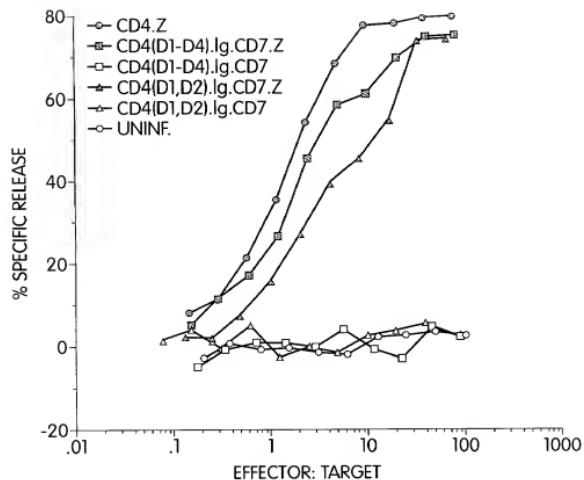


Fig. 21

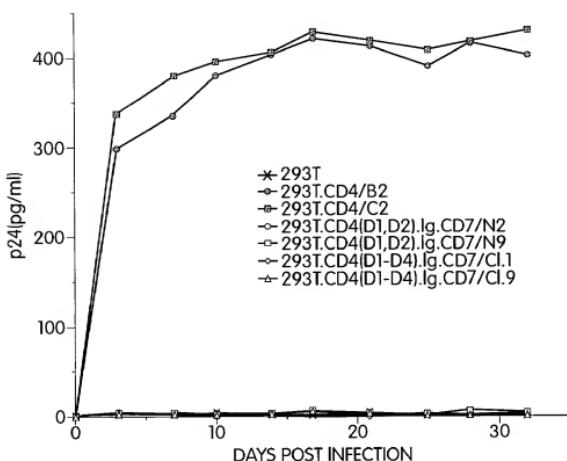


Fig. 22

## D1 - D4 of CD4

## Nucleic Acid Sequence

GCCTGTTTGA GAAGCAGCGG GCAAGAAAGA CGCAAGCCCA GAGGCCCTGC 51  
 CATTCTGTG GGCTCAGGTC CCTACTGGCT CAGGCCCTG CCTCCCTCG 101  
 CAAGGCCACA ATGAAACCGGG GAGTCCTTT TAGGCACTTG CTTCTGGTGC 151  
 TGCAACTGGC GCTCCCTCCA GCAGCCACTC AGGGAAACAA AGTGGTGCTG 201  
 GGCAAAAGGG GGGATACAGT GGAACTGACC TGATCAGCTT CCCAGAAAGA 251  
 GAGCATACAA TTCCACTGG AAAACTCCAA CCAGATAAAG ATTCTGGGAA 301  
 ATCAGGGCTC CTTCTTAACT AAGGGTCCAT CCAAGCTGAA TGATCGGCT 351  
 GACTCAAGAA GAAGCTTTG GGACCAAGGA AACTCCCCC TGATCATCAA 401  
 GAATCTTAAG ATAGAAGACT CAGATACTTA CATCTGTGAA GTGGAGGAC 451  
 AGAAGGAGGA GGTGCAATTG CTAGTGTTCG GATTGACTGTC CAACTCTGAC 501  
 ACCCCACTGC TTCAAGGGCA GAGCCCTGACC CTGACCTTGG AGAGCCCCC 551  
 TGGTAGTAGC CCCTCAGTGC AATGTTAGGAG TCCAAGGGGT AAAAACATAC 601  
 AGGGGGGAA GACCTCTCC GTGCTCAGC TGGAGCTCCA GGATAGTGGC 651  
 ACCTGGACAT GCACTGTCTT GCAGAACCCAG AAGAAGGTGG AGTTCAAAT 701  
 AGACATCGTG GTGCTAGCTT TCCAGAAGGC CTCCAGCATA GTCTATAAGA 751  
 AAGAGGGGGA ACAGCTGGAG TTCTCCCTTC CACTCGCCCTT TACAGTTGAA 801  
 AAGCTGACGG GCAGTGGCAG CAGTGGTGG CAGGGGAGA GGGCTTCCTC 851  
 CTCCAAGTCT TGGATCACCT TTGACCTGAA GAACAGGAA GTGTCTGTAA 901  
 AACGGGTTAC CCAGGACCCCT AAGCTCCAGA TGGGAAGGAA GCTCCCGCTC 951  
 CACCTCACCC TGCCCCAGGC CTTGCCCTAG TATGCTGGCT CTGGAAACCT 1001  
 CACCCCTGGCC CTTGAAGCGA AAACAGGAAA GTTGCATCAG GAAGTGAACCC 1051  
 TGGTGGTGTAG GAGAGCCACT CAGCTCCAGA AAAATTGAC CTGTGAGGTG 1101  
 TGGGGACCCA CCTCCCTAA GCTGATGCTG AGCTTGAACAC TGGAGAACAA 1151  
 GGAGGCAAAG GTCTCGAAGC GGGAGAAGCC GTGTGGGTG CTGAACCTG 1201  
 AGGCGGGGAT GTGGCAGTGT CTGCTGAGTG ACTCGGGACA GGTCCCTGCTG 1251  
 GAATCCAACA TCAAGTTCT GCCCACATGG TCCACCCCGG TGACACGGGA 1301  
 TCCC (SEQ ID NO: 28)

## Amino Acid Sequence

MNRGVFPRHL LLVLQLALLP AATQGNKVVL GKKGDTVELT CTASQKKSIQ 51  
 FHWKNSNQIK ILGNQGSFLT KGFSKLNDRA DSRRSLWDQG NFPLIINKL 101  
 IEDSDTYICE VEDQKEEVQL LVFGLTANSR THLLQGQSLT LTLESPPGSS 151  
 PSVQCRSPRG KNIQGGKTLR VSQLELQDSC TWTCTVLQNQ KKVEFKIDIV 201  
 VLAFKASSI VYKKEGEQVE FSFPLAFTVE KLTGSGELWW QAERASSSKS 251  
 WITFDLKNKE VSVKRVTDQP KLQMGKYLPL HLTLQPALPQ YAGSGNLTLA 301  
 LEAKTGLHQ EVNLVVMRAT QLQKNLTCVE WGPTSPKMLM SLKLENKEAK 351  
 VSKREKPVWV LNPEAGMWQC LLSDSGQVLL ESNIKVLPTW STPVHADP  
 (SEQ ID NO: 29)

Fig. 23

## D1 - D2 of CD4

## Nucleic Acid Sequence

GCCTGTTGA GAAAGCAGCGG GCAAGAAAAGA CGCAAGCCCCA GAGGCCCTGC 51  
 CATTCTGTG GGCTCAGGTC CCTACTGGCT CAGGCCCTG CCTCCCTCGG 101  
 CAAGGCCACA ATGAACCGGG GAGTCCCTTT TAGGCACTTG CTTCTGGTGC 151  
 TGCAACTGGC GCTCCCTCCA GCAGGCCACTC AGGGAAACAA AGTGGTGC 201  
 GGCAAAAAAAG GGGATACAGT GGAACGTGACC TGTACAGCTT CCCAGAAGAA 251  
 GAGCATACAA TTCCACTGGG AAAACTCCAA CCAAGATAAAAG ATTCTGGGAA 301  
 ATCAGGGCTC CTTCTTAACT AAAGGTCCAT CCAAGCTGAA TGATCCCGCT 351  
 GACTCAAGAA GAAGCCTTTG GGACCAAGGA AACTTCCCCC TGATCATCAA 401  
 GAATCTTAAG ATAGAAGACT CAGATACTTA CATCTGTGAA GTGGAGGACC 451  
 AGAAGGAGGA GGTGCAATTG CTAGTGTTCG GATTGACTGC CAACTCTGAC 501  
 ACCCAGCTGC TTCAGGGGC GAGCCTGACC CTGACCTTGG AGAGCCCCCCC 551  
 TGGTAGTAGC CCCTCACTGTC AATGTAGGAG TCCAAGGGGGT AAAAACATAC 601  
 AGGGGGGGAA GACCCCTCTCC GTGTCTCAGC TGGAGCTCCA GGATAGTGGC 651  
 ACCTGGACAT GCACTGTCTT GCAGAACAG AAGAAGGTGG AGTTCAAAAT 701  
 AGACATCGTG GTGCTAGCT (SEQ ID NO: 30)

## Amino Acid Sequence

MNRGVPFRHL LLVLQLALLP AATQGNKVVL GKKGDTVELT CTASQKKSIQ 51  
 FHWKNSNQIK ILGNQGSFLT KGPSKLNDRA DSRRSLWDQG NFPLIINKNLK 101  
 IEDSDTYICE VEDQKEEVQL LVFGLTANSR THLHQGQSLT LTLESPPGSS 151  
 PSVQCRSPRG KNIQGGKTLS VSQLELQDSDG TWTCTVLQNZ KKVEFKIDIV 201  
 VLA (SEQ ID NO: 31)

Fig. 24

## Hinge, CH2, and CH3 Domains of Human IgG1

## Nucleic Acid Sequence

GCTAGCAGAG CCCAAATCTT GTGACAAAAC TCACACATGC CCACCGTGCC 51  
 CAGCACCTGA ACTCTTGGGG GGACCGTCAG TCTTCCTCTT CCCCCCAAAA 101  
 CCCAAGGACA CCCTCATGAT CTCCCGGACC CCTGAGGTCA CATGCGTGGT 151  
 GGTGGACGTG AGCCACGAAG ACCCTGAGGT CAAGTTCAAC TGGTACGTGG 201  
 ACGGCGTGGA GGTGCATAAT GCCAAGACAA AGCCGCGGGA GGAGCAGTAC 251  
 AACAGCACGT ACCGGGTGGT CAGCGTCCTC ACCGTCCTGC ACCAGGACTG 301  
 GCTGAATGGC AAGGAGTACA AGTGCAGGT CTCCAACAAA GCCCTCCAG 351  
 CCCCCATCGA GAAAACCATC TCCAAAGCCA AAGGGCAGCC CCGAGAACCA 401  
 CAGGTGTACA CCCTGCCCCC ATCCCGGGAT GAGCTGACCA AGAACCGAGT 451  
 CAGCCTGACC TGCTTGGTCA AAGGCTTCTA TCCCCAGCGAC ATCGCCGTGG 501  
 AGTGGGAGAG CAATGGGCAG CCGGAGAACAA ACTACAAGAC CACGCCCTCCC 551  
 GTGCTGGACT CCGACGGCTC CTCTCTTCCTC TACAGCAAGC TCACCGTGG 601  
 CAAGAGCAGG TGGCAGCAGG GGAACGTCCTT CTCTATGCTCC GTGATGCATG 651  
 AGGCTCTGCA CAACCACTAC ACGCAGAAAGA GCCTCCCT GTCTCCGGGG 701  
 CTGCAACTGG ACGAGACCTG TGCTGAGGCC CAGGACGGGG AGCTGGACGG 751  
 GCTCTGGACG ACGGATCC (SEQ ID NO: 32)

## Amino Acid Sequence

EPKSCDKTHT CPPCPAPELL GGPSVFLFPP KPKDTLMISR TPEVTCVVVD 51  
 VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ YNSTYRVVSV LTVLHQDWLN 101  
 GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR DELTKNQVSL 151  
 TCLVKGFYPS DIAVEWESNG QPENNYKTP PVLDSDGSFF LYSKLTVDKS 201  
 RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GLQLDETCAE AQDGEGLGLW 251  
 TTDP (SEQ ID NO: 33)

Fig. 25

## CD7 Transmembrane Domain

## Nucleic Acid Sequence

CCAAGGGCCT CTGCCCTCCC TGCCCCACCG ACAGGCTCCG CCCTCCCTGA 51  
 CCCGCAGACA GCCTCTGCCC TCCCTGACCC GCCAGCAGCC TCTGCCCTCC 101  
 CTGCGGCCCT GGCGGTGATC TCCCTCCTCC TCAGGGCTGGG CCTGGGGGTG 151  
 GCGTGTGTGC TGGCGAGGAC GCGT (SEQ ID NO: 34)

## Amino Acid Sequence

PRASALPAPP TGSALPDPQT ASALPDPPAA SALPAALAVI SFLLGLGLGV 51  
 ACVLARTR (SEQ.ID NO: 35)

Fig. 26

## Zeta Intracellular Domain

## Nucleic Acid Sequence

ACGCGTTCA GCAGGAGCGC AGAGCCCCCC CGCTTACAGC AGGGCCAGAA 51  
 CCAGCTCTAT AACGAGCTCA ATCTAGGACG AAGAGAGGGAG TACCGATGTTT 101  
 TGGACAAGAG ACGTGGCCGG GACCCTGAGA TGGGGGGAAA GCCGAGAAAGG 151  
 AAGAACCTCT AGGAAGGCCT GTACAATGAA CTGCAGAAAG ATAAGATGGC 201  
 GGAGGGCTAC AGTGAGATTG GGATGAAAGG CGAGCGCCGG AGGGGCAAGG 251  
 GGCACGATGG CCTTTACCAAG GGTCTCAGTA CAGCCACCAA GGACACCTAC 301  
 GACGCCCTTC ACATGCAGGC CCTGCCCTCG CGCTAAAGCG GCCGC  
 (SEQ ID NO: 36)

## Amino Acid Sequence

TRFSRSAEPP AYQQGQNQLY NELNLRREE YDVLDKRRGR DPEMGGKPRR 51  
 KNPQEGLYNE LQKDKMAEA Y SEIGMYGERR RGKGHDGLYO GLSTATKDTY 101  
 DALHMQALPP R (SEQ ID NO: 37)

Fig. 27